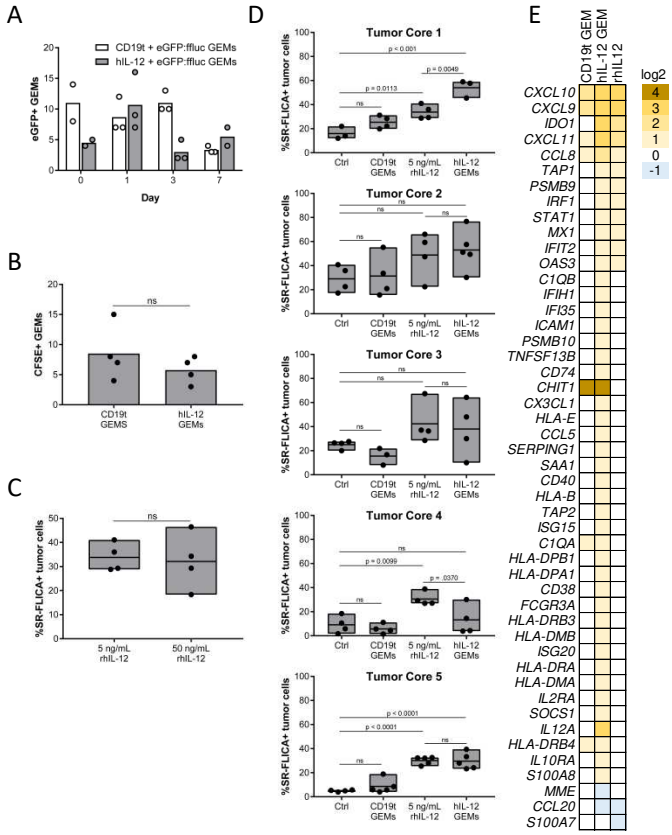

Supplementary Figure 6 hIL-12 GEMs induce IFNγ responses and solid tumor death in the absence of T cell proliferation in *ex vivo* human tumor slice culture. (A) CD19t and hIL-12 GEMs were co-transduced to express eGFP:ffluc and quantified by live fluorescent imaging (n = 1 tumor core, 1 experiment). Bars represent mean (SD) of 2-4 high-powered fields (HPFs)/slice, 1 slice/day. (B) CFSE-stained CD19t and hIL-12 GEMs were quantified by live imaging on day 6 of co-culture with slice. Data points represent individual HPFs quantified from 1 slice/treatment (n = 1 tumor core, 1 experiment). (C) Tumor cell death quantified by live fluorescent imaging 3 days after the addition of rhIL-12. Data points represent individual HPFs quantified from a single slice per treatment (n = 1 tumor core, 1 experiment). The mean of the 4 HPF data points shown here is represented as a single data point in Fig. 6C for the 5 ng/mL rhIL-12 group. (B,C) Statistical significance determined by an unpaired two-tailed t test. (D) Individual tumor core data from Fig. 6C. Data points represent individual HPFs quantified from a single slice/treatment (n = 5 tumor cores from 5 independent experiments). Statistical analysis by one-way ANOVA with Sidak's multiple comparisons test for the depicted pairwise comparisons. (E) Same data presented in Fig. 6F with the exclusion of RNA from tumor core 3. Heat map represents log2 fold change compared to PBS group, fold change values were averaged from three independent experiments. ns: p>0.05.